

BCS 04-5002-PCT\_Erhöhte Akt. OK1\_SEQUENZPROTO KOLL.ST25  
SEQUENCE LISTING

<110> Bayer CropScience GmbH

<120> Plants with increased activity of a starch phosphorylating enzyme

<130> BCS 04-5002-PCT

<150> EP04090086.2

<151> 2004-03-05

<150> US60/549,945

<151> 2004-03-05

<150> US60/549,945 provisional

<151> 2004-03-05

<150> EP04090121.7

<151> 2004-03-29

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 3591

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(3591)

<223>

**<400> 1**

Seite 2

## BCS 04-5002-PCT\_Erhöhte Akt. OK1\_SEQUENZPROTOKOLL.ST25

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tct gca att tat ttg aag tgg ata aac aca ggt cag att cct tgt ttt Ser Ala Ile Tyr Leu Lys Trp Ile Asn Thr Gly Gln Ile Pro Cys Phe 290 295 300	912
gaa gat gga ggg cat cac cgt cca aac agg cat gcc gag att tcc aga Glu Asp Gly Gly His His Arg Pro Asn Arg His Ala Glu Ile Ser Arg 305 310 315 320	960
ctt ata ttc cgt gag ttg gag cac att tgc agt aag aaa gat gct act Leu Ile Phe Arg Glu Leu Glu His Ile Cys Ser Lys Lys Asp Ala Thr 325 330 335	1008
cca gag gaa gtg ctt gtt gct cgg aaa atc cat ccg tgt tta cct tct Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser 340 345 350	1056
ttc aaa gca gag ttt act gca gct gtc cct cta act cgg att agg gac Phe Lys Ala Glu Phe Thr Ala Ala Val Pro Leu Thr Arg Ile Arg Asp 355 360 365	1104
ata gcc cat cgg aat gat att cct cat gat ctc aag caa gaa atc aag Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys 370 375 380	1152
cat acg ata caa aat aag ctt cac cgg aat gct ggt cca gaa gat cta His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu 385 390 395 400	1200
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## BCS 04-5002-PCT\_Erhöhte Akt. OK1\_SEQUENZPROTOKOLL.ST25

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ggt Gly	cta Leu	tct Ser	ggt Gly 580	tgg Trp	aag Lys	caa Gln	gaa Glu	gaa Glu 585	tgt Cys	tta Leu	gcc Ala	att Ile	gga Gly 590	aat Asn	gaa Glu	1776
ctc Leu	ctt Leu	gct Ala 595	tgg Trp	cga Arg	gaa Glu	agg Arg	gac Asp 600	cta Leu	ctt Leu	gaa Glu	aaa Lys	gaa Glu 605	ggg Gly	gaa Glu	gag Glu	1824
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gca Ala 625	cgc Arg	aga Arg	tta Leu	aca Thr	gca Ala 630	gaa Glu	tat Tyr	tct Ser	gat Asp	ttg Leu 635	ctt Leu	ctt Leu	caa Gln	ata Ile	ttt Phe 640	1920
cct Pro	cct Pro	aat Asn	gtg Val	gag Glu 645	att Ile	tta Leu	gga Gly	aaa Lys	gct Ala 650	cta Leu	gga Gly	att Ile	cca Pro	gag Glu 655	aat Asn	1968
agt Ser	gtc Val	aag Lys	acc Thr 660	tat Tyr	aca Thr	gaa Glu	gca Ala	gag Glu 665	att Ile	cgt Arg	gct Ala	gga Gly	att Ile 670	att Ile	ttc Phe	2016
cag Gln	atc Ile	tca Ser 675	aag Lys	ctc Leu	tgc Cys	act Thr	gtt Val 680	ctt Leu	cta Leu	aaa Lys	gct Ala	gta Val 685	aga Arg	aat Asn	tca Ser	2064
ctt Leu	ggt Gly 690	tct Ser	gag Glu	ggc Gly	tgg Trp	gat Asp 695	gtc Val	gtt Val	gta Val	cct Pro	gga Gly 700	tcg Ser	acg Thr	tct Ser	ggg Gly	2112
aca Thr 705	tta Leu	gtt Val	cag Gln	gtt Val	gag Glu 710	agc Ser	att Ile	gtt Val	ccg Pro	gga Gly 715	tca Ser	ttg Leu	cca Pro	gca Ala	act Thr 720	2160
tct Ser	ggt Gly	ggt Gly	cct Pro	att Ile 725	att Ile	ctc Leu	ttg Leu	gtc Val	aat Asn 730	aaa Lys	gct Ala	gat Asp	ggc Gly	gat Asp 735	gaa Glu	2208
gag Glu	gta Val	agt Ser	gct Ala 740	gct Ala	aat Asn	ggg Gly	aac Asn	ata Ile 745	gct Ala	gga Gly	gtc Val	atg Met	ctt Leu 750	ctg Leu	cag Gln	2256
gag Glu	ctg Leu	cct Pro 755	cac His	ttg Leu	tct Ser	cac His	ctt Leu 760	ggc Gly	gtt Val	aga Arg	gcg Ala	cgg Arg 765	cag Gln	gag Glu	aaa Lys	2304
att Ile	gtc Val 770	ttt Phe	gtg Val	aca Thr	tgt Cys	gat Asp 775	gat Asp	gat Asp	gac Asp	aag Lys	gtt Val 780	gct Ala	gat Asp	ata Ile	cga Arg	2352
cga Arg 785	ctt Leu	gtg Val	gga Gly	aaa Lys	ttt Phe 790	gtg Val	agg Arg	ttg Leu	gaa Glu	gca Ala 795	tct Ser	cca Pro	agt Ser	cat His	gtg Val 800	2400
aat Asn	ctg Leu	ata Ile	ctt Leu	tca Ser 805	act Thr	gag Glu	ggt Gly	agg Arg	agt Ser 810	cgc Arg	act Thr	tcc Ser	aaa Lys	tcc Ser 815	agt Ser	2448

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tct tcc aat agc ctc ctt tac tct tcc aag gat atc cct agt gga gga Ser Ser Asn Ser Leu Leu Tyr Ser Ser Lys Asp Ile Pro Ser Gly Gly 850 855 860	2592
atc ata gca ctt gct gat gca gat gta cca act tct ggt tca aaa tct Ile Ile Ala Leu Ala Asp Ala Asp Val Pro Thr Ser Gly Ser Lys Ser 865 870 875 880	2640
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agt cca gct gat ccg gac agt aac ctt gtg gaa gcc gag atc gct Ser Pro Ala Asp Pro Asp Ser Asn Leu Val Glu Ala Glu Ile Ala 1070 1075 1080	3249

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gct ttc gca aac ttc agc gaa gag ctt ctt gtg tca gga aca ggt	3384
Ala Phe Ala Asn Phe Ser Glu Glu Leu Leu Val Ser Gly Thr Gly	
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Lys Arg Leu Thr Val Asp Ser Val Phe Arg Gln Gln Leu Gly Gln	
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gtt cag tca agg cca caa cct ctg tag	3591
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1190 1195	

&lt;210&gt; 2

&lt;211&gt; 1196

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;400&gt; 2

Met Glu Ser Ile Gly Ser His Cys Cys Ser Ser Pro Phe Thr Phe Ile  
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Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser  
 35 40 45

Arg Leu Thr Cys Thr Ala Thr Ser Ser Ser Thr Ile Glu Glu Gln Arg  
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Lys Lys Lys Asp Gly Ser Gly Thr Lys Val Arg Leu Asn Val Arg Leu  
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Asp His Gln Val Asn Phe Gly Asp His Val Ala Met Phe Gly Ser Ala  
 85 90 95

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Lys Glu Ile Gly Ser Trp Lys Lys Lys Ser Pro Leu Asn Trp Ser Glu  
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 Asn Gly Trp Val Cys Glu Leu Glu Leu Asp Gly Gly Gln Val Leu Glu  
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 Tyr Lys Phe Val Ile Val Lys Asn Asp Gly Ser Leu Ser Trp Glu Ser  
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 Gly Asp Asn Arg Val Leu Lys Val Pro Asn Ser Gly Asn Phe Ser Val  
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 Val Cys His Trp Asp Ala Thr Arg Glu Thr Leu Asp Leu Pro Gln Glu  
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 Val Gly Asn Asp Asp Asp Val Gly Asp Gly Gly His Glu Arg Asp Asn  
 180 185 190  
 His Asp Val Gly Asp Asp Arg Val Val Gly Ser Glu Asn Gly Ala Gln  
 195 200 205  
 Leu Gln Lys Ser Thr Leu Gly Gly Gln Trp Gln Gly Lys Asp Ala Ser  
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 Phe Met Arg Ser Asn Asp His Gly Asn Arg Glu Val Gly Arg Asn Trp  
 225 230 235 240  
 Asp Thr Ser Gly Leu Glu Gly Thr Ala Leu Lys Met Val Glu Gly Asp  
 245 250 255  
 Arg Asn Ser Lys Asn Trp Trp Arg Lys Leu Glu Met Val Arg Glu Val  
 260 265 270  
 Ile Val Gly Ser Val Glu Arg Glu Glu Arg Leu Lys Ala Leu Ile Tyr  
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 Ser Ala Ile Tyr Leu Lys Trp Ile Asn Thr Gly Gln Ile Pro Cys Phe  
 290 295 300  
 Glu Asp Gly Gly His His Arg Pro Asn Arg His Ala Glu Ile Ser Arg  
 305 310 315 320  
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 325 330 335  
 Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser  
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 Phe Lys Ala Glu Phe Thr Ala Ala Val Pro Leu Thr Arg Ile Arg Asp  
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Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys  
 370 375 380  
 His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu  
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 Ile Ala Thr Glu Ala Met Leu Gln Arg Ile Thr Glu Thr Pro Gly Lys  
 405 410 415  
 Tyr Ser Gly Asp Phe Val Glu Gln Phe Lys Ile Phe His Asn Glu Leu  
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 Lys Asp Phe Phe Asn Ala Gly Ser Leu Thr Glu Gln Leu Asp Ser Met  
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 Glu Cys Lys Lys Arg Leu Asp Thr Ser Gly Glu Ser Ser Asn Val Leu  
 465 470 475 480  
 Glu Leu Ile Lys Thr Met His Ser Leu Ala Ser Leu Arg Glu Thr Ile  
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 Ile Lys Glu Leu Asn Ser Gly Leu Arg Asn Asp Ala Pro Asp Thr Ala  
 500 505 510  
 Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Gly Leu Glu Asp  
 515 520 525  
 Tyr Phe Phe Val Leu Leu Ser Arg Phe Leu Asn Ala Leu Glu Thr Met  
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 Gly Gly Ala Asp Gln Leu Ala Lys Asp Val Gly Ser Arg Asn Val Ala  
 545 550 555 560  
 Ser Trp Asn Asp Pro Leu Asp Ala Leu Val Leu Gly Val His Gln Val  
 565 570 575  
 Gly Leu Ser Gly Trp Lys Gln Glu Glu Cys Leu Ala Ile Gly Asn Glu  
 580 585 590  
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 595 600 605  
 Asp Gly Lys Thr Ile Trp Ala Met Arg Leu Lys Ala Thr Leu Asp Arg  
 610 615 620  
 Ala Arg Arg Leu Thr Ala Glu Tyr Ser Asp Leu Leu Leu Gln Ile Phe  
 625 630 635 640



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Pro Pro Asn Val Glu Ile Leu Gly Lys Ala Leu Gly Ile Pro Glu Asn  
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 Ser Val Lys Thr Tyr Thr Glu Ala Glu Ile Arg Ala Gly Ile Ile Phe  
 660 665 670  
 Gln Ile Ser Lys Leu Cys Thr Val Leu Leu Lys Ala Val Arg Asn Ser  
 675 680 685  
 Leu Gly Ser Glu Gly Trp Asp Val Val Val Pro Gly Ser Thr Ser Gly  
 690 695 700  
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 705 710 715 720  
 Ser Gly Gly Pro Ile Ile Leu Leu Val Asn Lys Ala Asp Gly Asp Glu  
 725 730 735  
 Glu Val Ser Ala Ala Asn Gly Asn Ile Ala Gly Val Met Leu Leu Gln  
 740 745 750  
 Glu Leu Pro His Leu Ser His Leu Gly Val Arg Ala Arg Gln Glu Lys  
 755 760 765  
 Ile Val Phe Val Thr Cys Asp Asp Asp Lys Val Ala Asp Ile Arg  
 770 775 780  
 Arg Leu Val Gly Lys Phe Val Arg Leu Glu Ala Ser Pro Ser His Val  
 785 790 795 800  
 Asn Leu Ile Leu Ser Thr Glu Gly Arg Ser Arg Thr Ser Lys Ser Ser  
 805 810 815  
 Ala Thr Lys Lys Thr Asp Lys Asn Ser Leu Ser Lys Lys Lys Thr Asp  
 820 825 830  
 Lys Lys Ser Leu Ser Ile Asp Asp Glu Glu Ser Lys Pro Gly Ser Ser  
 835 840 845  
 Ser Ser Asn Ser Leu Leu Tyr Ser Ser Lys Asp Ile Pro Ser Gly Gly  
 850 855 860  
 Ile Ile Ala Leu Ala Asp Ala Asp Val Pro Thr Ser Gly Ser Lys Ser  
 865 870 875 880  
 Ala Ala Cys Gly Leu Leu Ala Ser Leu Ala Glu Ala Ser Ser Lys Val  
 885 890 895  
 His Ser Glu His Gly Val Pro Ala Ser Phe Lys Val Pro Thr Gly Val  
 900 905 910

## BCS 04-5002-PCT\_Erhöhte Akt. OK1\_SEQUENZPROTOKOLL.ST25

Val Ile Pro Phe Gly Ser Met Glu Leu Ala Leu Lys Gln Asn Asn Ser  
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 Glu Glu Lys Phe Ala Ser Leu Leu Glu Lys Leu Glu Thr Ala Arg Pro  
 930 935 940  
 Glu Gly Gly Glu Leu Asp Asp Ile Cys Asp Gln Ile His Glu Val Met  
 945 950 955 960  
 Lys Thr Leu Gln Val Pro Lys Glu Thr Ile Asn Ser Ile Ser Lys Ala  
 965 970 975  
 Phe Leu Lys Asp Ala Arg Leu Ile Val Arg Ser Ser Ala Asn Val Glu  
 980 985 990  
 Asp Leu Ala Gly Met Ser Ala Ala Gly Leu Tyr Glu Ser Ile Pro Asn  
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 1025 1030 1035  
 Ala Ala Gly Val Ser Gln Arg Glu Ala Ser Met Ala Val Leu Val  
 1040 1045 1050  
 Gln Glu Met Leu Ser Pro Asp Leu Ser Phe Val Leu His Thr Val  
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 Ser Pro Ala Asp Pro Asp Ser Asn Leu Val Glu Ala Glu Ile Ala  
 1070 1075 1080  
 Pro Gly Leu Gly Glu Thr Leu Ala Ser Gly Thr Arg Gly Thr Pro  
 1085 1090 1095  
 Trp Arg Leu Ala Ser Gly Lys Leu Asp Gly Ile Val Gln Thr Leu  
 1100 1105 1110  
 Ala Phe Ala Asn Phe Ser Glu Glu Leu Leu Val Ser Gly Thr Gly  
 1115 1120 1125  
 Pro Ala Asp Gly Lys Tyr Val Arg Leu Thr Val Asp Tyr Ser Lys  
 1130 1135 1140  
 Lys Arg Leu Thr Val Asp Ser Val Phe Arg Gln Gln Leu Gly Gln  
 1145 1150 1155  
 Arg Leu Gly Ser Val Gly Phe Phe Leu Glu Arg Asn Phe Gly Cys  
 1160 1165 1170

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Val Gln Ser Arg Pro Gln Pro Leu  
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		1				5					10				
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Gly Gly Arg Pro Arg Arg Gly Leu Val Leu Pro Pro Pro Gly Val Gly															
15 20 25															
gcg ggt gtg ctg ctc cgc cgg gga gcg atg gcg ctc cct ggg cgg cgc	147														
Ala Gly Val Leu Leu Arg Arg Gly Ala Met Ala Leu Pro Gly Arg Arg															
30 35 40 45															
ggc ttc gcg tgc cgc ggg aga tcc gcg gcc tcg gcg gca gag aga aca	195														
Gly Phe Ala Cys Arg Gly Arg Ser Ala Ala Ser Ala Ala Glu Arg Thr															
50 55 60															
aag gag aaa aag aga aga gat tct tca aag cag cca ttg gtg cat ctc	243														
Lys Glu Lys Lys Arg Arg Asp Ser Ser Lys Gln Pro Leu Val His Leu															
65 70 75															
cag gtt tgt cta gag cac cag gtt aag ttt ggt gag cat gta ggc att	291														
Gln Val Cys Leu Glu His Gln Val Lys Phe Gly Glu His Val Gly Ile															
80 85 90															
atc ggt tcc aca aag gag ctt ggt tca tgg gag gag cag gtt gaa ctg	339														
Ile Gly Ser Thr Lys Glu Leu Gly Ser Trp Glu Glu Gln Val Glu Leu															
95 100 105															
gaa tgg act aca aat ggt tgg gtc tgc cag ctt aag ctc cct gga gaa	387														
Glu Trp Thr Thr Asn Gly Trp Val Cys Gln Leu Lys Leu Pro Gly Glu															
110 115 120 125															
aca ctt gtg gag ttt aaa ttt gtt ata ttt ttg gtg gga gga aaa gat	435														
Thr Leu Val Glu Phe Lys Phe Val Ile Phe Leu Val Gly Gly Lys Asp															
130 135 140															
aaa ata tgg gaa gat ggt aat aac cgt gtt gtt gag ctg ccg aag gat	483														

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gaa Glu	ctt Leu 175	tta Leu	gga Gly	aca Thr	cca Pro	aag Lys 180	ttt Phe	gag Glu	ttg Leu	gtc Val	gga Gly 185	gaa Glu	gct Ala	gaa Glu	aag Lys	579
aat Asn 190	act Thr	ggc Gly	gag Glu	gat Asp	gct Ala 195	tca Ser	gca Ala	tct Ser	gta Val	act Thr 200	ttt Phe	gca Ala	cct Pro	gaa Glu	aaa Lys 205	627
gtt Val	caa Gln	gat Asp	att Ile	tca Ser 210	gtt Val	gtt Val	gag Glu	aat Asn	ggt Gly 215	gat Asp	cca Pro	gca Ala	cca Pro	gag Glu 220	gcc Ala	675
gag Glu	tca Ser	agc Ser	aaa Lys 225	ttt Phe	ggt Gly	ggg Gly	caa Gln	tgg Trp 230	caa Gln	gga Gly	agt Ser	aaa Lys	act Thr 235	gtt Val	ttc Phe	723
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aca Thr	act Thr 255	ggg Gly	ctt Leu	gat Asp	gga Gly	ata Ile 260	gca Ala	ctg Leu	aaa Lys	ctg Leu	gtg Val 265	gag Glu	ggc Gly	gat Asp	aaa Lys	819
gca Ala 270	tcc Ser	agg Arg	aac Asn	tgg Trp	tgg Trp 275	cgg Arg	aag Lys	tta Leu	gag Glu	gtt Val 280	gtt Val	cgc Arg	ggg Gly	ata Ile	ttg Leu 285	867
tca Ser	gaa Glu	tct Ser	ttt Phe	gat Asp 290	gac Asp	cag Gln	agt Ser	cgt Arg	ctg Leu 295	ggg Gly	gcc Ala	ctt Leu	gta Val	tac Tyr 300	tca Ser	915
gct Ala	att Ile	tat Tyr	ctg Leu 305	aag Lys	tgg Trp	att Ile	tat Tyr	aca Thr 310	ggt Gly	cag Gln	ata Ile	tcg Ser	tgc Cys 315	ttt Phe	gaa Glu	963
gat Asp	ggt Gly	ggc Gly 320	cac His	cat His	cgg Arg	cct Pro	aac Asn 325	aaa Lys	cat His	gct Ala	gag Glu	ata Ile 330	tcg Ser	agg Arg	caa Gln	1011
ata Ile	ttc Phe 335	cgt Arg	gaa Glu	ctt Leu	gaa Glu	atg Met 340	atg Met	tat Tyr	tat Tyr	ggg Gly	aaa Lys 345	acc Thr	aca Thr	tca Ser	gcc Ala	1059
aag Lys 350	gat Asp	gtt Val	ctc Leu	gtg Val	att Ile 355	cgc Arg	aaa Lys	att Ile	cat His	ccc Pro 360	ttt Phe	tta Leu	cct Pro	tca Ser	ttt Phe 365	1107
aag Lys	tca Ser	gag Glu	ttt Phe	aca Thr 370	gcc Ala	tct Ser	gtc Val	cct Pro	cta Leu 375	aca Thr	cga Arg	att Ile	cgt Arg	gat Asp 380	att Ile	1155
gct Ala	cac His	cgg Arg	aat Asn 385	gac Asp	atc Ile	cca Pro	cat His	gat Asp 390	ctc Leu	aag Lys	caa Gln	gaa Glu	atc Ile 395	aag Lys	cat His	1203
act Thr	ata Ile	caa Gln 400	aac Asn	aaa Lys	ctt Leu	cat His	cgt Arg 405	aat Asn	gct Ala	gga Gly	cct Pro	gag Glu 410	gat Asp	ctt Leu	att Ile	1251
gct Ala	aca Ser	gaa Glu	gtc Leu	atg Met	ctt Leu	gct Ala	agg Arg	att Ile	act Thr	aag Lys	acc Thr	cct Pro	gga Glu	gaa Glu	tac Ser	1299

BCS 04-5002-PCT_Erhöhte Akt. OK1_SEQUENZPROTOKOLL.ST25																
Ala 415	Thr	Glu	Val	Met	Leu	Ala 420	Arg	Ile	Thr	Lys	Thr 425	Pro	Gly	Glu	Tyr	
agt Ser 430	gaa Glu	aca Thr	ttt Phe	gtt Val	gaa Glu 435	caa Gln	ttc Phe	acg Thr	ata Ile	ttt Phe 440	tat Tyr	agc Ser	gaa Glu	cta Leu	aaa Lys 445	1347
gat Asp	ttc Phe	ttc Phe	aat Asn	gct Ala 450	ggc Gly	agc Ser	cta Leu	ttt Phe	gag Glu 455	caa Gln	ctg Leu	gag Glu	tcc Ser	atc Ile 460	aag Lys	1395
gaa Glu	tct Ser	ctg Leu	aac Asn 465	gag Glu	tca Ser	ggc Gly	tta Leu	gaa Glu 470	gtt Val	ctc Leu	tca Ser	tcc Ser	ttt Phe 475	gtg Val	gaa Glu	1443
acc Thr	aaa Lys	agg Arg 480	agt Ser	ttg Leu	gac Asp	caa Gln	gtg Val 485	gat Asp	cat His	gca Ala	gaa Glu	gat Asp 490	ttg Leu	gat Asp	aaa Lys	1491
aat Asn 495	gat Asp	acc Thr	att Ile	caa Gln	att Ile 500	ttg Leu	atg Met	act Thr	acc Thr	ttg Leu	caa Gln 505	tca Ser	tta Leu	tct Ser	tct Ser	1539
cta Leu 510	aga Arg	tcg Ser	gtt Val	cta Leu	atg Met 515	aag Lys	ggc Gly	ctt Leu	gaa Glu	agt Ser 520	ggc Gly	ctt Leu	aga Arg	aat Asn	gat Asp 525	1587
gcg Ala	cct Pro	gat Asp	aat Asn	gct Ala 530	ata Ile	gca Ala	atg Met	cga Arg	caa Gln 535	aag Lys	tgg Trp	cgc Arg	ctt Leu	tgt Cys 540	gaa Glu	1635
att Ile	agt Ser	ctt Leu	gag Glu 545	gat Asp	tat Tyr	tca Ser	ttt Phe	gtt Val 550	ctg Leu	tta Leu	agc Ser	aga Arg	ttc Phe 555	atc Ile	aat Asn	1683
act Thr	ctt Leu	gaa Glu 560	gcc Ala	tta Leu	ggc Gly	gga Gly	tca Ser 565	gct Ala	tca Ser	ctt Leu	gca Ala 570	aag Lys	gat Asp	gta Val	gct Ala	1731
aga Arg	aat Asn 575	act Thr	act Thr	cta Leu	tgg Trp	gat Asp 580	act Thr	act Thr	ctt Leu	gat Asp	gcc Ala 585	ctt Leu	gtc Val	att Ile	ggc Gly	1779
atc Ile 590	aat Asn	caa Gln	gtt Val	agc Ser	ttt Phe 595	tca Ser	ggc Gly	tgg Trp	aaa Lys	aca Thr 600	gat Asp	gaa Glu	tgt Cys	att Ile	gcc Ala 605	1827
ata Ile	ggg Gly	aat Asn	gag Glu	att Ile 610	ctt Leu	tcc Ser	tgg Trp	aag Lys	caa Gln 615	aaa Lys	ggc Gly	cta Leu	tct Ser	gaa Glu 620	agt Ser	1875
gaa Glu	ggc Gly	tgt Cys	gaa Glu 625	gat Asp	ggg Gly	aaa Lys	tat Tyr	att Ile 630	tgg Trp	tca Ser	cta Leu	aga Arg	ctt Leu 635	aaa Lys	gct Ala	1923
aca Thr	ctg Leu	gac Asp 640	aga Arg	gca Ala	cgg Arg	aga Arg	tta Leu 645	acg Thr	gaa Glu	gag Glu	tac Tyr	tct Ser 650	gaa Glu	gca Ala	ctt Leu	1971
ctt Leu 655	tct Ser	ata Ile	ttc Phe	cct Pro	gaa Glu 660	aaa Lys	gta Val	atg Met	gtt Val	att Ile	ggg Gly 665	aaa Lys	gcc Ala	ctt Leu	gga Gly	2019
ata Ile 670	cca Pro	gat Asp	aac Asn	agt Ser	gtg Val 675	aga Arg	act Thr	tac Tyr	aca Thr	gag Glu 680	gca Ala	gaa Glu	att Ile	cgt Arg	gct Ala 685	2067
ggc att	att gtt	ttt cag	gta tct	aaa cta	tgc aca	gta ctt	cag aaa	gca gta	ctt cag	aaa gca	ctt cag	aaa gca	ctt cag	aaa gca	ctt cag	2115

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Gly	Ile	Val	Phe	Gln	Val	Ser	Lys	Leu	Cys	Thr	Val	Leu	Gln	Lys	Ala
				690					695					700	
att	cga	gaa	gta	ctt	gga	tca	act	ggc	tgg	gat	gtt	ctt	gtt	cct	gga
Ile	Arg	Glu	Val	Leu	Gly	Ser	Thr	Gly	Trp	Asp	Val	Leu	Val	Pro	Gly
			705					710					715		
gtg	gcc	cat	gga	act	ctg	atg	cgg	gtg	gaa	aga	att	ctt	cct	gga	tca
Val	Ala	His	Gly	Thr	Leu	Met	Arg	Val	Glu	Arg	Ile	Leu	Pro	Gly	Ser
			720				725					730			
tta	cct	tca	tct	gtc	aaa	gaa	cct	gtg	gtt	cta	att	gta	gat	aag	gct
Leu	Pro	Ser	Ser	Val	Lys	Glu	Pro	Val	Val	Leu	Ile	Val	Asp	Lys	Ala
	735					740					745				
gat	gga	gat	gaa	gag	gtc	aaa	gct	gct	ggg	gat	aat	ata	gtt	ggt	gtt
Asp	Gly	Asp	Glu	Glu	Val	Lys	Ala	Ala	Gly	Asp	Asn	Ile	Val	Gly	Val
				755						760					765
att	ctt	ctt	cag	gaa	cta	cct	cac	ctt	tca	cat	ctt	ggt	gtt	aga	gct
Ile	Leu	Leu	Gln	Glu	Leu	Pro	His	Leu	Ser	His	Leu	Gly	Val	Arg	Ala
				770					775					780	
cgt	caa	gag	aat	gtt	gta	ttt	gta	act	tgt	gaa	tat	gat	gac	aca	gtt
Arg	Gln	Glu	Asn	Val	Val	Phe	Val	Thr	Cys	Glu	Tyr	Asp	Asp	Thr	Val
			785					790					795		
aca	gat	gtg	tat	ttg	ctt	gag	gga	aaa	tat	atc	aga	tta	gaa	gca	tca
Thr	Asp	Val	Tyr	Leu	Leu	Glu	Gly	Lys	Tyr	Ile	Arg	Leu	Glu	Ala	Ser
			800				805					810			
tcc	atc	aat	gtc	aat	ctc	tca	ata	gtt	tca	gaa	aaa	aat	gac	aat	gct
Ser	Ile	Asn	Val	Asn	Leu	Ser	Ile	Val	Ser	Glu	Lys	Asn	Asp	Asn	Ala
	815					820					825				
gtc	tct	aca	gaa	cca	aat	agt	aca	ggg	aat	cca	ttt	caa	cag	aaa	ctc
Val	Ser	Thr	Glu	Pro	Asn	Ser	Thr	Gly	Asn	Pro	Phe	Gln	Gln	Lys	Leu
					835					840					845
caa	aat	gaa	ttc	tct	cta	cca	tcg	gat	atc	gag	atg	cca	ctg	caa	atg
Gln	Asn	Glu	Phe	Ser	Leu	Pro	Ser	Asp	Ile	Glu	Met	Pro	Leu	Gln	Met
				850					855					860	
tct	aag	caa	aaa	agc	aaa	tca	gga	gtg	aat	ggt	agt	ttt	gct	gct	ctt
Ser	Lys	Gln	Lys	Ser	Lys	Ser	Gly	Val	Asn	Gly	Ser	Phe	Ala	Ala	Leu
			865					870					875		
gag	ctt	tca	gaa	gct	tca	gtg	gaa	tca	gct	ggt	gca	aaa	gct	gct	gca
Glu	Leu	Ser	Glu	Ala	Ser	Val	Glu	Ser	Ala	Gly	Ala	Lys	Ala	Ala	Ala
			880				885					890			
tgc	aga	act	ctt	tct	gtt	ctt	gct	tca	ttg	tct	aat	aaa	gtc	tat	agt
Cys	Arg	Thr	Leu	Ser	Val	Leu	Ala	Ser	Leu	Ser	Asn	Lys	Val	Tyr	Ser
	895					900					905				
gat	caa	gga	gtt	cca	gca	gcc	ttt	aga	gtc	cct	tct	ggt	gct	gtg	ata
Asp	Gln	Gly	Val	Pro	Ala	Ala	Phe	Arg	Val	Pro	Ser	Gly	Ala	Val	Ile
					915					920					925
cca	ttt	gga	tca	atg	gag	gat	gcg	ctc	aag	aaa	agt	gga	tca	ctg	gaa
Pro	Phe	Gly	Ser	Met	Glu	Asp	Ala	Leu	Lys	Lys	Ser	Gly	Ser	Leu	Glu
				930					935					940	
tcc	ttt	aca	agc	ctt	cta	gaa	aag	att	gaa	aca	gcc	aaa	gtc	gaa	aat
Ser	Phe	Thr	Ser	Leu	Leu	Glu	Lys	Ile	Glu	Thr	Ala	Lys	Val	Glu	Asn
			945					950					955		
ggt	gaa	gtt	gat	agc	ctg	gcg	ttg	gag	cta	caa	gca	ata	att	tca	cat

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Gly	Glu	Val	Asp	Ser	Leu	Ala	Leu	Glu	Leu	Gln	Ala	Ile	Ile	Ser	His	
		960					965					970				
ctt	tcc	cca	ccg	gag	gag	act	att	ata	ttt	ctc	aaa	aga	atc	ttc	cca	2979
Leu	Ser	Pro	Pro	Glu	Glu	Thr	Ile	Ile	Phe	Leu	Lys	Arg	Ile	Phe	Pro	
	975					980					985					
cag	gat	gtc	cgg	ttg	att	ggt	aga	tct	agt	gct	aat	gtg	gag	gat	ttg	3027
Gln	Asp	Val	Arg	Leu	Ile	Val	Arg	Ser	Ser	Ala	Asn	Val	Glu	Asp	Leu	
990					995					1000					1005	
gct	ggt	atg	tca	gct	gct	ggt	ctc	tat	gat	tca	att	ccc	aat	gtc		3072
Ala	Gly	Met	Ser	Ala	Ala	Gly	Leu	Tyr	Asp	Ser	Ile	Pro	Asn	Val		
				1010					1015					1020		
agt	ctc	atg	gac	cca	tgt	gcc	ttt	gga	gct	gcg	ggt	ggg	aag	gtt		3117
Ser	Leu	Met	Asp	Pro	Cys	Ala	Phe	Gly	Ala	Ala	Val	Gly	Lys	Val		
				1025					1030					1035		
tgg	gct	tct	tta	tac	aca	agg	aga	gcc	atc	cta	agc	cgt	cga	gcc		3162
Trp	Ala	Ser	Leu	Tyr	Thr	Arg	Arg	Ala	Ile	Leu	Ser	Arg	Arg	Ala		
				1040					1045					1050		
gct	ggt	gtt	tat	cag	aga	gac	gcg	aca	atg	gct	gtt	ctt	gtc	caa		3207
Ala	Gly	Val	Tyr	Gln	Arg	Asp	Ala	Thr	Met	Ala	Val	Leu	Val	Gln		
				1055					1060					1065		
gaa	ata	ctg	cag	cca	gat	ctc	tcc	ttc	gtg	ctt	cat	act	gtt	tgc		3252
Glu	Ile	Leu	Gln	Pro	Asp	Leu	Ser	Phe	Val	Leu	His	Thr	Val	Cys		
				1070					1075					1080		
ccc	gct	gac	cat	gac	ccc	aag	gtt	gtc	cag	gct	gag	gtc	gcc	cct		3297
Pro	Ala	Asp	His	Asp	Pro	Lys	Val	Val	Gln	Ala	Glu	Val	Ala	Pro		
				1085					1090					1095		
ggg	ctg	ggt	gaa	acg	ctt	gct	tca	gga	acc	cgt	ggc	acc	ccg	tgg		3342
Gly	Leu	Gly	Glu	Thr	Leu	Ala	Ser	Gly	Thr	Arg	Gly	Thr	Pro	Trp		
				1100					1105					1110		
agg	ctg	tca	tgt	aac	aaa	ttc	gat	gga	aaa	gtt	gcc	act	ctt	gcc		3387
Arg	Leu	Ser	Cys	Asn	Lys	Phe	Asp	Gly	Lys	Val	Ala	Thr	Leu	Ala		
				1115					1120					1125		
ttt	tca	aat	ttc	agt	gag	gag	atg	gtg	gtg	cac	aac	tct	ggt	cct		3432
Phe	Ser	Asn	Phe	Ser	Glu	Glu	Met	Val	Val	His	Asn	Ser	Gly	Pro		
				1130					1135					1140		
gcc	aat	gga	gaa	gta	att	cgt	ctt	act	gtt	gat	tac	agc	aag	aag		3477
Ala	Asn	Gly	Glu	Val	Ile	Arg	Leu	Thr	Val	Asp	Tyr	Ser	Lys	Lys		
				1145					1150					1155		
cca	ttg	tcg	gtt	gat	aca	acc	ttt	agg	aag	cag	ttt	ggt	cag	cga		3522
Pro	Leu	Ser	Val	Asp	Thr	Thr	Phe	Arg	Lys	Gln	Phe	Gly	Gln	Arg		
				1160					1165					1170		
ctg	gct	gcg	att	ggc	cag	tat	ctg	gag	cag	aag	ttc	ggg	agt	gca		3567
Leu	Ala	Ala	Ile	Gly	Gln	Tyr	Leu	Glu	Gln	Lys	Phe	Gly	Ser	Ala		
				1175					1180					1185		
cag	gat	gtg	gaa	ggt	tgc	ctg	gtt	ggg	aaa	gat	att	ttt	ata	gtg		3612
Gln	Asp	Val	Glu	Gly	Cys	Leu	Val	Gly	Lys	Asp	Ile	Phe	Ile	Val		
				1190					1195					1200		
caa	agc	agg	cca	cag	cca	tag	aagccgaatt	c								3644
Gln	Ser	Arg	Pro	Gln	Pro											
				1205												

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 <210> 4  
 <211> 1206  
 <212> PRT  
 <213> Oryza sativa

<400> 4

Met Thr Ser Leu Arg Pro Leu Glu Thr Ser Leu Ser Ile Gly Gly Arg  
 1 5 10 15  
 Pro Arg Arg Gly Leu Val Leu Pro Pro Pro Gly Val Gly Ala Gly Val  
 20 25 30  
 Leu Leu Arg Arg Gly Ala Met Ala Leu Pro Gly Arg Arg Gly Phe Ala  
 35 40 45  
 Cys Arg Gly Arg Ser Ala Ala Ser Ala Ala Glu Arg Thr Lys Glu Lys  
 50 55 60  
 Lys Arg Arg Asp Ser Ser Lys Gln Pro Leu Val His Leu Gln Val Cys  
 65 70 75 80  
 Leu Glu His Gln Val Lys Phe Gly Glu His Val Gly Ile Ile Gly Ser  
 85 90 95  
 Thr Lys Glu Leu Gly Ser Trp Glu Glu Gln Val Glu Leu Glu Trp Thr  
 100 105 110  
 Thr Asn Gly Trp Val Cys Gln Leu Lys Leu Pro Gly Glu Thr Leu Val  
 115 120 125  
 Glu Phe Lys Phe Val Ile Phe Leu Val Gly Gly Lys Asp Lys Ile Trp  
 130 135 140  
 Glu Asp Gly Asn Asn Arg Val Val Glu Leu Pro Lys Asp Gly Lys Phe  
 145 150 155 160  
 Asp Ile Val Cys His Trp Asn Arg Thr Glu Glu Pro Leu Glu Leu Leu  
 165 170 175  
 Gly Thr Pro Lys Phe Glu Leu Val Gly Glu Ala Glu Lys Asn Thr Gly  
 180 185 190  
 Glu Asp Ala Ser Ala Ser Val Thr Phe Ala Pro Glu Lys Val Gln Asp  
 195 200 205  
 Ile Ser Val Val Glu Asn Gly Asp Pro Ala Pro Glu Ala Glu Ser Ser  
 210 215 220



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Lys Phe Gly Gly Gln Trp Gln Gly Ser Lys Thr Val Phe Met Arg Ser  
 225 230 235 240

Asn Glu His Leu Asn Lys Glu Ala Asp Arg Met Trp Asp Thr Thr Gly  
 245 250 255

Leu Asp Gly Ile Ala Leu Lys Leu Val Glu Gly Asp Lys Ala Ser Arg  
 260 265 270

Asn Trp Trp Arg Lys Leu Glu Val Val Arg Gly Ile Leu Ser Glu Ser  
 275 280 285

Phe Asp Asp Gln Ser Arg Leu Gly Ala Leu Val Tyr Ser Ala Ile Tyr  
 290 295 300

Leu Lys Trp Ile Tyr Thr Gly Gln Ile Ser Cys Phe Glu Asp Gly Gly  
 305 310 315 320

His His Arg Pro Asn Lys His Ala Glu Ile Ser Arg Gln Ile Phe Arg  
 325 330 335

Glu Leu Glu Met Met Tyr Tyr Gly Lys Thr Thr Ser Ala Lys Asp Val  
 340 345 350

Leu Val Ile Arg Lys Ile His Pro Phe Leu Pro Ser Phe Lys Ser Glu  
 355 360 365

Phe Thr Ala Ser Val Pro Leu Thr Arg Ile Arg Asp Ile Ala His Arg  
 370 375 380

Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys His Thr Ile Gln  
 385 390 395 400

Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu Ile Ala Thr Glu  
 405 410 415

Val Met Leu Ala Arg Ile Thr Lys Thr Pro Gly Glu Tyr Ser Glu Thr  
 420 425 430

Phe Val Glu Gln Phe Thr Ile Phe Tyr Ser Glu Leu Lys Asp Phe Phe  
 435 440 445

Asn Ala Gly Ser Leu Phe Glu Gln Leu Glu Ser Ile Lys Glu Ser Leu  
 450 455 460

Asn Glu Ser Gly Leu Glu Val Leu Ser Ser Phe Val Glu Thr Lys Arg  
 465 470 475 480

Ser Leu Asp Gln Val Asp His Ala Glu Asp Leu Asp Lys Asn Asp Thr  
 485 490 495

BCS 04-5002-PCT\_Erhöhte Akt. OK1\_SEQUENZPROTOKOLL.ST25  
 Ile Gln Ile Leu Met Thr Thr Leu Gln Ser Leu Ser Ser Leu Arg Ser  
 500 505 510

Val Leu Met Lys Gly Leu Glu Ser Gly Leu Arg Asn Asp Ala Pro Asp  
 515 520 525

Asn Ala Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Ser Leu  
 530 535 540

Glu Asp Tyr Ser Phe Val Leu Leu Ser Arg Phe Ile Asn Thr Leu Glu  
 545 550 555 560

Ala Leu Gly Gly Ser Ala Ser Leu Ala Lys Asp Val Ala Arg Asn Thr  
 565 570 575

Thr Leu Trp Asp Thr Thr Leu Asp Ala Leu Val Ile Gly Ile Asn Gln  
 580 585 590

Val Ser Phe Ser Gly Trp Lys Thr Asp Glu Cys Ile Ala Ile Gly Asn  
 595 600 605

Glu Ile Leu Ser Trp Lys Gln Lys Gly Leu Ser Glu Ser Glu Gly Cys  
 610 615 620

Glu Asp Gly Lys Tyr Ile Trp Ser Leu Arg Leu Lys Ala Thr Leu Asp  
 625 630 635 640

Arg Ala Arg Arg Leu Thr Glu Glu Tyr Ser Glu Ala Leu Leu Ser Ile  
 645 650 655

Phe Pro Glu Lys Val Met Val Ile Gly Lys Ala Leu Gly Ile Pro Asp  
 660 665 670

Asn Ser Val Arg Thr Tyr Thr Glu Ala Glu Ile Arg Ala Gly Ile Val  
 675 680 685

Phe Gln Val Ser Lys Leu Cys Thr Val Leu Gln Lys Ala Ile Arg Glu  
 690 695 700

Val Leu Gly Ser Thr Gly Trp Asp Val Leu Val Pro Gly Val Ala His  
 705 710 715 720

Gly Thr Leu Met Arg Val Glu Arg Ile Leu Pro Gly Ser Leu Pro Ser  
 725 730 735

Ser Val Lys Glu Pro Val Val Leu Ile Val Asp Lys Ala Asp Gly Asp  
 740 745 750

Glu Glu Val Lys Ala Ala Gly Asp Asn Ile Val Gly Val Ile Leu Leu  
 755 760 765

BCS 04-5002-PCT\_Erhöhte Akt. OK1 SEQUENZPROTOKOLL.ST25  
 Gln Glu Leu Pro His Leu Ser His Leu Gly Val Arg Ala Arg Gln Glu  
 770 775 780  
 Asn Val Val Phe Val Thr Cys Glu Tyr Asp Asp Thr Val Thr Asp Val  
 785 790 795 800  
 Tyr Leu Leu Glu Gly Lys Tyr Ile Arg Leu Glu Ala Ser Ser Ile Asn  
 805 810 815  
 Val Asn Leu Ser Ile Val Ser Glu Lys Asn Asp Asn Ala Val Ser Thr  
 820 825 830  
 Glu Pro Asn Ser Thr Gly Asn Pro Phe Gln Gln Lys Leu Gln Asn Glu  
 835 840 845  
 Phe Ser Leu Pro Ser Asp Ile Glu Met Pro Leu Gln Met Ser Lys Gln  
 850 855 860  
 Lys Ser Lys Ser Gly Val Asn Gly Ser Phe Ala Ala Leu Glu Leu Ser  
 865 870 875 880  
 Glu Ala Ser Val Glu Ser Ala Gly Ala Lys Ala Ala Ala Cys Arg Thr  
 885 890 895  
 Leu Ser Val Leu Ala Ser Leu Ser Asn Lys Val Tyr Ser Asp Gln Gly  
 900 905 910  
 Val Pro Ala Ala Phe Arg Val Pro Ser Gly Ala Val Ile Pro Phe Gly  
 915 920 925  
 Ser Met Glu Asp Ala Leu Lys Lys Ser Gly Ser Leu Glu Ser Phe Thr  
 930 935 940  
 Ser Leu Leu Glu Lys Ile Glu Thr Ala Lys Val Glu Asn Gly Glu Val  
 945 950 955 960  
 Asp Ser Leu Ala Leu Glu Leu Gln Ala Ile Ile Ser His Leu Ser Pro  
 965 970 975  
 Pro Glu Glu Thr Ile Ile Phe Leu Lys Arg Ile Phe Pro Gln Asp Val  
 980 985 990  
 Arg Leu Ile Val Arg Ser Ser Ala Asn Val Glu Asp Leu Ala Gly Met  
 995 1000 1005  
 Ser Ala Ala Gly Leu Tyr Asp Ser Ile Pro Asn Val Ser Leu Met  
 1010 1015 1020  
 Asp Pro Cys Ala Phe Gly Ala Ala Val Gly Lys Val Trp Ala Ser  
 1025 1030 1035

BCS 04-5002-PCT\_Erhöhte Akt. OK1\_SEQUENZPROTOKOLL.ST25  
 Leu Tyr Thr Arg Arg Ala Ile Leu Ser Arg Arg Ala Ala Gly Val  
 1040 1045 1050

Tyr Gln Arg Asp Ala Thr Met Ala Val Leu Val Gln Glu Ile Leu  
 1055 1060 1065

Gln Pro Asp Leu Ser Phe Val Leu His Thr Val Cys Pro Ala Asp  
 1070 1075 1080

His Asp Pro Lys Val Val Gln Ala Glu Val Ala Pro Gly Leu Gly  
 1085 1090 1095

Glu Thr Leu Ala Ser Gly Thr Arg Gly Thr Pro Trp Arg Leu Ser  
 1100 1105 1110

Cys Asn Lys Phe Asp Gly Lys Val Ala Thr Leu Ala Phe Ser Asn  
 1115 1120 1125

Phe Ser Glu Glu Met Val Val His Asn Ser Gly Pro Ala Asn Gly  
 1130 1135 1140

Glu Val Ile Arg Leu Thr Val Asp Tyr Ser Lys Lys Pro Leu Ser  
 1145 1150 1155

Val Asp Thr Thr Phe Arg Lys Gln Phe Gly Gln Arg Leu Ala Ala  
 1160 1165 1170

Ile Gly Gln Tyr Leu Glu Gln Lys Phe Gly Ser Ala Gln Asp Val  
 1175 1180 1185

Glu Gly Cys Leu Val Gly Lys Asp Ile Phe Ile Val Gln Ser Arg  
 1190 1195 1200

Pro Gln Pro  
 1205

<210> 5

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<212> PRT

<213> Arabidopsis thaliana, Oryza sativa

<400> 5

Leu Pro His Leu Ser His Leu Gly Val Arg Ala Arg  
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